CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 60 amino acids that has at least 55% identity based on the Clustal method of alignment when compared to a delta-6 desaturase polypeptide of SEQ ID NO:2, a second nucleotide sequence encoding a first polypeptide of at least 114 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a sphingolipid desaturase polypeptide of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:17 or a third nucleotide sequence comprising the complement of the first or second nucleotide sequences.

2. The isolated polynucleotide of Claim 1, wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, and 16 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, and 17.

3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.

4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.

5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.

6. An isolated host cell comprising the chimeric gene of Claim 5.

7. An isolated host cell comprising an isolated polynucleotide of Claim 1 or Claim 3.

8. The isolated host cell of Claim 7 wherein the isolated host is selected from the group consisting of yeast, bacteria, plant, and virus.

9. A virus comprising the isolated polynucleotide of Claim 1.

10. A polypeptide of at least 60 amino acids that has at least 55% identity based on the Clustal method of alignment when compared to the polypeptide of SEQ ID NO:2, or at least 114 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:17.

11. A method of selecting an isolated polynucleotide that affects the level of expression of a desaturase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, and 16 and the complement of such nucleotide sequences;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of a polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the isolated polynucleotide.

12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, and 16 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, and 17.

13. A method of selecting an isolated polynucleotide that affects the level of expression of a delta-6 desaturase or sphingolipid desaturase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide of Claim 1;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the polynucleotide.

14. A method of obtaining a nucleic acid fragment encoding a delta-6 desaturase or sphingolipid desaturase polypeptide comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 40 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, and 16 and the complement of such nucleotide sequences; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15. A method of obtaining a nucleic acid fragment encoding the amino acid sequence encoding a delta-6 desaturase or sphingolipid desaturase polypeptide comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, and 16 and the complement of such nucleotide sequences;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

16. A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the chimeric gene of Claim 5; and

(b) growing the transformed host cell under conditions suitable for the expression of the chimeric gene allowing expression of the polynucleotide in an amount to alter the concentration of fatty acids with delta-6 double bonds in the host cell to provide a positive selection means.

17. The method of Claim 16 wherein the host cell is selected from the group consisting of plant cells and procaryotes.

18. The method of Claim 16 wherein levels of tariric acid are altered.

19. A method for positive selection of a transformed cell comprising:

(a) transforming a plant cell with the chimeric gene of Claim 5;

(b) growing a plant from the transformed plant cell of step (a) allowing expression of the polynucleotide in an amount to alter the concentration of fatty acids with delta-6 double bonds in the seeds of the plant to provide a positive selection means.

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